SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
                COHEN, MAURICE
                COLPITTS, TRACEY L.
                FRIEDMAN, PAULA N.
                GORDON, JULIAN
                GRANADOS, EDWARD N.
                HODGES, STEVEN C.
                KLASS, MICHAEL R.
                KRATOCHVIL, JON D.
                ROBERTS-RAPP, LISA
                RUSSELL, JOHN C.
                STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
        FOR DETECTING DISEASES OF THE PROSTATE

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Abbott Laboratories
  (B) STREET: 100 Abbott Park Road
  (C) CITY: Abbott Park
  (D) STATE: IL
  (E) COUNTRY: USA
  (F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER: 08/850,713
  (B) FILING DATE: 02-MAY-1997

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Becker, Cheryl L.
  (B) REGISTRATION NUMBER: 35,441
  (C) REFERENCE/DOCKET NUMBER: 6083.US.P1

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 847/935-1729
  (B) TELEFAX: 847/938-2623
  (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 258 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGGGCTGTAC CAGGGCGTGC CCAGAGCTGA GCCGGGCACC GAGGCCCGGA GACACTATGA    60
TGAAGGCGTT CGGATGGGCA GCCTGGGGCT GTTCCTGCAG TGCGCCATCT CCCTGGTCTT   120
CTCTCTGGTC ATGGACCGGC TGGTGCAGCG ATTCGGCACT CGAGCAGTCT ATTTGGCCAG   180
TGTGGCAGCT TTCCCTGTGG CTGCCGGTGC CACATGCCTG TCCCACAGTG TGGCCGTGGT   240
GACAGCTTCA GCCGCCTT                                                 258
```

    (2) INFORMATION FOR SEQ ID NO:2:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 217 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
ACCAGGGCGT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT GATGAAGGCG    60
TTCGGATGGG CAGCCTGGGG CTGTTCCTGC AGTGCGCCAT CTCCCTGGTC TTCTCTCTGG   120
TCATGGACCG GCTGGTGCAG CGATTCGGCA CTCGAGCAGT CTATTTGGCC AGTGTGGCAG   180
CTTTCCCTGT GGCTGCCGGT GCCACATGCC TGTCCCA                            217
```

    (2) INFORMATION FOR SEQ ID NO:3:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 255 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ix) FEATURE:
    (A) NAME/KEY: base_polymorphism
    (B) LOCATION: 215
    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
        T or C polymorphism at this position"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GACAGCTTCA GCCGCCCTCA CCGGGTTCAC CTTCTCAGCC CTGCAGATCC TGCCCTACAC    60
ACTGGCCTCC CTCTACCACC GGGAGAAGCA GGTGTTCCTG CCCAAATACC GAGGGGACAC   120
TGGAGGTGCT AGCAGTGAGG ACAGCCTGAT GACCAGCTTC CTGCCAGGCC CTAAGCCTGG   180
AGCTCCCTTC CCTAATGGAC ACGTGGGTGC TGGANGCAGT GGCCTGCTCC CACCTCCACC   240
CGCGCTCTGC GGGGC                                                    255
```

    (2) INFORMATION FOR SEQ ID NO:4:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 247 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GCTCCCTTCC CTAATGGACA CGTGGGTGCT GGAGGCAGTG GCCTGCTCCC ACCTCCACCC        60
GCGCTCTGCG GGGCCTCTGC CTGTGATGTC TCCGTACGTG TGGTGGTGGG TGAGCCCACC       120
GAGGCCAGGG TGGTTCCGGG CCGGGGCATC TGCCTGGACC TCGCCATCCT GGATAGTGCC       180
TTCCTGCTGT CCCAGGTGGC CCCATCCCTG TTTATGGGCT CCATTGTCCA GCTCAGCCAG       240
TCTGTCA                                                                 247
```

        (2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 231 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
TGGATAGTGC CTTCCTGCTG TCCCAGGTGG CCCCATCCCT GTTTATGGGC TCCATTGTCC        60
AGCTCAGCCA GTCTGTCACT GCCTATATGG TGTCTGCCGC AGGCTGGGTC TGGTCGCCAT       120
TTACTTTGCT ACACAGGTAG TATTTGACAA GAGCGACTTG GCCAAATACT CAGCGTAGAA       180
AACTTCCAGC ACATTGGGGT GGAGGGCCTG CCTCACTGGG TCCCAGCTCC C               231
```

        (2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 195 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:
            (A) NAME/KEY: base_polymorphism
            (B) LOCATION: 178
            (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                T or C polymorphism at this position"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
CTTGGCCAAA TACTCAGCGT AGAAAACTTC CAGCACATTG GGGTGGAGGG CCTGCCTCAC        60
TGGGTCCCAG CTCCCCGCTC CTGTTAGCCC CATGGGGCTG CCGGGCTGGC CGCCAGTTTC       120
TGTTGCTGCC AAAGTAATGT GGCTCTCTGC TGCCACCCTG TGCTGCTGAG GTGCGTANTG       180
CACAGCTGGG GGCTG                                                        195
```

        (2) INFORMATION FOR SEQ ID NO:7:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 223 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:
            (A) NAME/KEY: base_polymorphism
            (B) LOCATION: 67
            (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                T or C polymorphism at this position"

        (ix) FEATURE:
            (A) NAME/KEY: base_polymorphism
            (B) LOCATION: 222
            (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                T or C polymorphism at this position"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GCCAGTTTCT GTTGCTGCCA AAGTAATGTG GCTCTCTGCT GCCACCCTGT GCTGCTGAGG        60
```

```
TGCGTANTGC ACAGCTGGGG GCTGGGGCGT CCCTCTCCTC TCTCCCCAGT CTCTAGGGCT    120
GCCTGACTGG AGGCCTTCCA AGGGGGTTTC AGTCTGGACT TATACAGGGA GGCCAGAAGG    180
GCTCCATGCA CTGGAATGCG GGGACTCTGC AGGTGGATTA CNC                      223
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 342 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (ix) FEATURE:
     (A) NAME/KEY: base_polymorphism
     (B) LOCATION: 323
     (D) OTHER INFORMATION: /note= "'N' represents an A or G or
         T or C polymorphism at this position"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GCCAGAAGGG CTCCATGCAC TGGAATGCGG GGACTCTGCA GGTGGATTAC CCAGGCTCAG     60
GGTTAACAGC TAGCCTCCTA GTTGAGACAC ACCTAGAGAA GGGTTTTTGG GAGCTGAATA    120
AACTCAGTCA CCTGGTTTCC CATCTCTAAG CCCCTTAACC TGCAGCTTCG TTTAATGTAG    180
CTCTTGCATG GGAGTTTCTA GGATGAAACA CTCCTCCATG GGATTTGAAC ATATGAAAGT    240
TATTTGTAGG GGAAGAGTCC TGAGGGGCAA CACACAAGAA CCAGGTCCCC TCAGCCCACA    300
GCACTGTCTT TTTGCTGATC CANCCCCCTC TTACTTTTAT CA                       342
```

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 265 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GGGGAAGAGT CCTGAGGGGC AACACACAAG AACCAGGTCC CCTCAGCCCA CAGCACTGTC     60
TTTTTGCTGA TCCACCCCCC TCTTACCTTT TATCAGGATG TGGCCTGTTG GTCCTTCTGT    120
TGCCATCACA GAGACACAGG CATTTAAATA TTTAACTTAT TTATTTAACA AAGTAGAAGG    180
GAATCCATTG CTAGCTTTTC TGTGTTGGTG TCTAATATTT GGGTAGGGTG GGGGATCCCC    240
AACAATCAGG TCCCCTGAGA TAGCT                                          265
```

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 288 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (ix) FEATURE:
     (A) NAME/KEY: base_polymorphism
     (B) LOCATION: 147
     (D) OTHER INFORMATION: /note= "'N' represents an A or G or
         T or C polymorphism at this position"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
CTCTTACCTT TTATCAGGAT GTGGCCTGTT GGTCCTTCTG TTGCCATCAC AGAGACACAG     60
GCATTTAAAT ATTTAACTTA TTTATTTAAC AAAGTAGAAG GGAATCCATT GCTAGCTTTT    120
CTGTGTTGGT GTCTAATATT TGGGTANGGT GGGGGATCCC CAACAATCAG GTCCCCTGAG    180
ATAGCTGGTC ATTGGGCTGA TCATTGCCAG AATCTTCTTC TCCTGGGGTC TGGCCCCCCA    240
AAATGCCTAA CCCAGGACCT TGGAAATTCT ACTCATCCCA AATGATAA                 288
```

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 272 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ix) FEATURE:
      (A) NAME/KEY: base_polymorphism
      (B) LOCATION: 216
      (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
AAATTCTACT CATCCCAAAT GATAATTCCA AATGCTGTTA CCCAAGGTTA GGGTGTTGAA    60
GGAAGGTAGA GGGTGGGGCT TCAGGTCTCA ACGGCTTCCC TAACCACCCC TCTTCTCTTG   120
GCCCAGCCTG GTTCCCCCCA CTTCCACTCC CCTCTACTCT CTCTAGGACT GGGCTGATGA   180
AGGCACTGCC CAAAATTTCC CCTACCCCCA ACTTTNCCCT ACCCCCAACT TTCCCCACCA   240
GCTCCACAAC CCTGTTTGGA GCTACTGCAG GT                                 272
```

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 294 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ix) FEATURE:
      (A) NAME/KEY: base_polymorphism
      (B) LOCATION: 18
      (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

    (ix) FEATURE:
      (A) NAME/KEY: base_polymorphism
      (B) LOCATION: 19
      (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

    (ix) FEATURE:
      (A) NAME/KEY: base_polymorphism
      (B) LOCATION: 197
      (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
AAGGCACTGC CCAAAATNNC CCCTACCCCC AACTTTCCCC TACCCCCAAC TTTCCCCACC    60
AGCTCCACAA CCCTGTTTGG AGCTACTGCA GGACCAGAAG CACAAAGTGC GGTTTCCCAA   120
GCCTTTGTCC ATCTCAGCCC CCAGAGTATA TCTGTGCTTG GGGAATCTCA CACAGAAACT   180
CAGGAGCACC CCCTGCNTGA GCTAAGGGAG GTCTTATCTC TCAGGGGGGG TTTAAGTGCC   240
GTTTGCAATA ATGTCGTCTT ATTTATTTAG CGGGGTGAAT ATTTTATACT GTAA         294
```

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 151 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ix) FEATURE:

```
                    (A) NAME/KEY: base_polymorphism
                    (B) LOCATION: 113
                    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                        T or C polymorphism at this position"

          (ix)  FEATURE:
                    (A) NAME/KEY: base_polymorphism
                    (B) LOCATION: 147
                    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                        T or C polymorphism at this position"

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:13:
```

CTCCACAACC CTGTTTGGAG CTACTGCAGG ACCAGAAGCA CAAAGTGCGG TTTCCCAAGC   60
CTTTGTCCAT CTCAGCCCCC AGAGTATATC TGTGCTTGGG GAATCTCACA CANAAACTCA   120
GGAGCACCCC CTGCCTGAGC TAAGGGNGGT C   151

```
                 (2) INFORMATION FOR SEQ ID NO:14:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 213 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
```

CCCAGAGTAT ATCTGTGCTT GGGGAATCTC ACACAGAAAC TCAGGAGCAC CCCCTGCCTG   60
AGCTAAGGGA GGTCTTATCT CTCAGGGGGG GTTTAAGTGC CGTTTGCAAT AATGTCGTCT   120
TATTTATTTA GCGGGGTGAA TATTTTATAC TGTAAGTGAG CAATCAGAGT ATAATGTTTA   180
TGGTGACAAA ATTAAAGGCT TTCTTATATG TTT   213

```
                 (2) INFORMATION FOR SEQ ID NO:15:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 2143 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
```

ACCAGGGCGT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT GATGAAGGCG   60
TTCGGATGGG CAGCCTGGGG CTGTTCCTGC AGTGCGCCAT CTCCCTGGTC TTCTCTCTGG   120
TCATGGACCG GCTGGTGCAG CGATTCGGCA CTCGAGCAGT CTATTTGGCC AGTGTGGCAG   180
CTTTCCCTGT GGCTGCCGGT GCCACATGCC TGTCCCACAG TGTGGCCGTG GTGACAGCTT   240
CAGCCGCCCT CACCGGGTTC ACCTTCTCAG CCCTGCAGAT CCTGCCCTAC ACACTGGCCT   300
CCCTCTACCA CCGGGAGAAG CAGGTGTTCC TGCCCAAATA CCGAGGGGAC ACTGGAGGTG   360
CTAGCAGTGA GGACAGCCTG ATGACCAGCT TCCTGCCAGG CCCTAAGCCT GGAGCTCCCT   420
TCCCTAATGG ACACGTGGGT GCTGGAGGCA GTGGCCTGCT CCCACCTCCA CCCGCGCTCT   480
GCGGGGCCTC TGCCTGTGAT GTCTCCGTAC GTGTGGTGGT GGGTGAGCCC ACCGAGGCCA   540
GGGTGGTTCC GGGCCGGGGC ATCTGCCTGG ACCTCGCCAT CCTGGATAGT GCCTTCCTGC   600
TGTCCCAGGT GGCCCCATCC CTGTTTATGG GCTCCATTGT CCAGCTCAGC CAGTCTGTCA   660
CTGCCTATAT GGTGTCTGCC GCAGGCCTGG GTCTGGTCGC CATTTACTTT GCTACACAGG   720
TAGTATTTGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAAACTTCC AGCACATTGG   780
GGTGGAGGGC CTGCCTCACT GGGTCCCAGC TCCCCGCTCC TGTTAGCCCC ATGGGGCTGC   840
CGGGCTGGCC GCCAGTTTCT GTTGCTGCCA AAGTAATGTG GCTCTCTGCT GCCACCCTGT   900
GCTGCTGAGG TGCGTAGCTG CACAGCTGGG GGCTGGGGCG TCCCTCTCCT CTCTCCCCAG   960
TCTCTAGGGC TGCCTGACTG GAGGCCTTCC AAGGGGGTTT CAGTCTGGAC TTATACAGGG 1020
AGGCCAGAAG GGCTCCATGC ACTGGAATGA GGGACTGCTGC AGGTGGATTA CCCAGGCTCA 1080
GGGTTAACAG CTAGCCTCCT AGTTGAGACA CACCTAGAGA AGGGTTTTTG GGAGCTGAAT 1140
AAACTCAGTC ACCTGGTTTC CCATCTCTAA GCCCCTTAAC CTGCAGCTTC GTTTAATGTA 1200
GCTCTTGCAT GGGAGTTTCT AGGATGAAAC ACTCCTCCAT GGGATTTGAA CATATGAAAG 1260
TTATTTGTAG GGGAAGAGTC CTGAGGGGCA ACACACAAGA ACCAGGTCCC CTCAGCCCAC 1320

```
AGCACTGTCT TTTTGCTGAT CCACCCCCCT CTTACCTTTT ATCAGGATGT GGCCTGTTGG    1380
TCCTTCTGTT GCCATCACAG AGACACAGGC ATTTAAATAT TTAACTTATT TATTTAACAA    1440
AGTAGAAGGG AATCCATTGC TAGCTTTTCT GTGTTGGTGT CTAATATTTG GGTAGGGTGG    1500
GGGATCCCCA ACAATCAGGT CCCCTGAGAT AGCTGGTCAT TGGGCTGATC ATTGCCAGAA    1560
TCTTCTTCTC CTGGGGTCTG GCCCCCCAAA ATGCCTAACC CAGGACCTTG GAAATTCTAC    1620
TCATCCCAAA TGATAATTCC AAATGCTGTT ACCCAAGGTT AGGGTGTTGA AGGAAGGTAG    1680
AGGGTGGGGC TTCAGGTCTC AACGGCTTCC CTAACCACCC CTCTTCTCTT GGCCCAGCCT    1740
GGTTCCCCCC ACTTCCACTC CCCTCTACTC TCTCTAGGAC TGGGCTGATG AAGGCACTGC    1800
CCAAAATTTC CCCTACCCCC AACTTTCCCC TACCCCCAAC TTTCCCCACC AGCTCCACAA    1860
CCCTGTTTGG AGCTACTGCA GGACCAGAAG CACAAAGTGC GGTTCCCAA GCCTTTGTCC     1920
ATCTCAGCCC CCAGAGTATA TCTGTGCTTG GGGAATCTCA CACAGAAACT CAGGAGCACC    1980
CCCTGCCTGA GCTAAGGGAG GTCTTATCTC TCAGGGGGGG TTTAAGTGCC GTTTGCAATA    2040
ATGTCGTCTT ATTTTTTTAG CGGGGTGAAT ATTTTATACT GTAAGTGAGC AATCAGAGTA    2100
TAATGTTTAT GGTGACAAAA TTAAAGGCTT TCTTATATGT TTA                      2143
```

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2152 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
GGGGCTGTAC CAGGGCGTGC CCAGAGCTGA GCCGGGCACC GAGGCCCGGA GACACTATGA    60
TGAAGGCGTT CGGATGGGCA GCCTGGGGCT GTTCCTGCAG TGCGCCATCT CCCTGGTCTT   120
CTCTCTGGTC ATGGACCGGC TGGTGCAGCG ATTCGGCACT CGAGCAGTCT ATTTGGCCAG   180
TGTGGCAGCT TTCCCTGTGG CTGCCGGTGC CACATGCCTG TCCCACAGTG TGGCCGTGGT   240
GACAGCTTCA GCCGCCCTCA CCGGGTTCAC CTTCTCAGCC CTGCAGATCC TGCCCTACAC   300
ACTGGCCTCC CTCTACCACC GGGAGAAGCA GGTGTTCCTG CCCAAATACC GAGGGGACAC   360
TGGAGGTGCT AGCAGTGAGG ACAGCCTGAT GACCAGCTTC CTGCCAGGCC CTAAGCCTGG   420
AGCTCCCTTC CCTAATGGAC ACGTGGGTGC TGGAGGCAGT GGCCTGCTCC CACCTCCACC   480
CGCGCTCTGC GGGGCCTCTG CCTGTGATGT CTCCGTACGT GTGGTGGTGG GTGAGCCCAC   540
CGAGGCCAGG GTGGTTCCGG GCCGGGGCAT CTGCCTGGAC CTCGCCATCC TGGATAGTGC   600
CTTCCTGCTG TCCCAGGTGG CCCCATCCCT GTTTATGGGC TCCATTGTCC AGCTCAGCCA   660
GTCTGTCACT GCCTATATGG TGTCTGCCGC AGGCCTGGGT CTGGTCGCCA TTTACTTTGC   720
TACACAGGTA GTATTTGACA AGAGCGACTT GGCCAAATAC TCAGCGTAGA AAACTTCCAG   780
CACATTGGGG TGGAGGGCCT GCCTCACTGG GTCCAGCTC CCCGCTCCTG TTAGCCCCAT    840
GGGGCTGCCG GGCTGGCCGC CAGTTTCTGT TGCTGCCAAA GTAATGTGGC TCTCTGCTGC   900
CACCCTGTGC TGCTGAGGTG CGTAGCTGCA CAGCTGGGGG CTGGGGCGTC CCTCTCCTCT   960
CTCCCCAGTC TCTAGGGCTG CCTGACTGGA GGCCTTCCAA GGGGGTTTCA GTCTGGACTT  1020
ATACAGGGAG GCCAGAAGGG CTCCATGCAC TGGAATGCGG GGACTCTGCA GGTGGATTAC  1080
CCAGGCTCAG GGTTAACAGC TAGCCTCCTA GTTGAGACAC ACCTAGAGAA GGGTTTTTGG  1140
GAGCTGAATA AACTCAGTCA CCTGGTTTCC CATCTCTAAG CCCCTTAACC TGCAGCTTCG  1200
TTTAATGTAG CTCTTGCATG GGAGTTTCTA GGATGAAACA CTCCTCCATG GGATTTGAAC  1260
ATATGAAAGT TATTTGTAGG GGAAGAGTCC TGAGGGGCAA CACACAAGAA CCAGGTCCCC  1320
TCAGCCCACA GCACTGTCTT TTTGCTGATC CACCCCCCTC TTACCTTTTA TCAGGATGTG  1380
GCCTGTTGGT CCTTCTGTTG CCATCACAGA GACACAGGCA TTTAAATATT TAACTTATTT  1440
ATTTAACAAA GTAGAAGGGA ATCCATTGCT AGCTTTTCTG TGTTGGTGTC TAATATTTGG  1500
GTAGGGTGGG GATCCCCAA CAATCAGGTC CCCTGAGATA GCTGGTCATT GGGCTGATCA   1560
TTGCCAGAAT CTTCTTCTCC TGGGGTCTGG CCCCCCAAAA TGCCTAACCC AGGACCTTGG  1620
AAATTCTACT CATCCCAAAT GATAATTCCA AATGCTGTTA CCCAAGGTTA GGGTGTTGAA  1680
GGAAGGTAGA GGGTGGGGCT TCAGGTCTCA ACGGCTTCCC TAACCACCCC TCTTCTCTTG  1740
GCCCAGCCTG GTTCCCCCCA CTTCCACTCC CCTCTACTCT CTCTAGGACT GGGCTGATGA  1800
AGGCACTGCC CAAAATTTCC CCTACCCCCA ACTTTCCCCT ACCCCCAACT TTCCCCACCA  1860
GCTCCACAAC CTGTTTGGA GCTACTGCAG GACCAGAAGC ACAAAGTGCG GTTCCCAAG   1920
CCTTTGTCCA TCTCAGCCCC CAGAGTATAT CTGTGCTTGG GGAATCTCAC ACAGAAACTC  1980
AGGAGCACCC CCTGCCTGAG CTAAGGGAGG TCTTATCTCT CAGGGGGGGT TTAAGTGCCG  2040
TTTGCAATAA TGTCGTCTTA TTTATTTAGC GGGGTGAATA TTTTATACTG TAAGTGAGCA  2100
ATCAGAGTAT AATGTTTATG GTGACAAAAT TAAAGGCTTT CTTATATGTT TA          2152
```

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 68 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC   60
CGGGAATT   68

          (2) INFORMATION FOR SEQ ID NO:18:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 68 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG   60
GAATTCCG   68

          (2) INFORMATION FOR SEQ ID NO:19:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCGGATAAC AATTTCACAC AGGA   24

          (2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGT   18

          (2) INFORMATION FOR SEQ ID NO:21:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGTTCCTGCC CAAATACC   18

          (2) INFORMATION FOR SEQ ID NO:22:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTCTGGTCG CCATTTAC   18

        (2) INFORMATION FOR SEQ ID NO:23:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGGCAACAC ACAAGAAC   18

        (2) INFORMATION FOR SEQ ID NO:24:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 19 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCAGCCCCCA GAGTATATC   19

        (2) INFORMATION FOR SEQ ID NO:25:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTCCATGCA CTGGAATG   18

        (2) INFORMATION FOR SEQ ID NO:26:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACCCAGGACC TTGGAAAT   18

        (2) INFORMATION FOR SEQ ID NO:27:

        (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACACCCTAAC CTTGGGTAAC   20

          (2) INFORMATION FOR SEQ ID NO:28:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTAGAAACT CCCATGCAAG   20

          (2) INFORMATION FOR SEQ ID NO:29:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TGGCAGCAAC AGAAACTG   18

          (2) INFORMATION FOR SEQ ID NO:30:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACTATCCAGG ATGGCGAG   18

          (2) INFORMATION FOR SEQ ID NO:31:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGATTGCTCA CTTACAGT   18

          (2) INFORMATION FOR SEQ ID NO:32:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGTTAGGGA AGCCGTTG   18

        (2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 18 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCCCAATGA CCAGCTAT   18

        (2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 22 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTCCAAATGC TGTTACCCAA GG   22

        (2) INFORMATION FOR SEQ ID NO:35:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 24 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTGCTCCTG AGTTTCTGTG TGAG   24

        (2) INFORMATION FOR SEQ ID NO:36:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 255 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg
1   5   10   15
Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser Leu Gly Leu Phe Leu
            20   25   30
Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val Met Asp Arg Leu Val
            35   40   45

```
Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser Val Ala Ala Phe
    50                  55                  60
Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser Val Ala Val Val
65                  70                  75                  80
Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile
                85                  90                  95
Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe
            100                 105                 110
Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser
            115                 120                 125
Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro
    130             135                 140
Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro
145             150                 155                 160
Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser Val Arg Val Val Val
            165                 170                 175
Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg Gly Ile Cys Leu
            180                 185                 190
Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro
        195                 200                 205
Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala
    210                 215                 220
Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala
225             230                 235                 240
Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
            245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 44 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr
1                   5                   10                  15
Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly
            20                  25                  30
Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 27 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg
1                   5                   10                  15
Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 27 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg
1   5   10   15
Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
            20   25

        (2) INFORMATION FOR SEQ ID NO:40:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 8 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asp Tyr Lys Asp Asp Asp Asp Lys
1   5

        (2) INFORMATION FOR SEQ ID NO:41:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 21 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1   5   10   15
His His His His His
            20